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Figure 1a (1)

Figure 1a (2)

Figure 1a (3)

Figure 1a (4)

# Protein Sequence Alignment

11/15/99						
ALIGNED SEQUENCES						
Reference molecule:	ureXCS1	1 -	226	( 226 aa)	Homology	
Sequence 2:	ureXkuka	1 -	226	( 226 aa)	100%	
Sequence 3:	ureXDS4	1 -	226	( 226 aa)	99%	
Sequence 4:	ureX2301	1 -	226	( 226 aa)	99%	
Sequence 5:	ureX390	1 -	226	( 226 aa)	99%	
Sequence 6:	A felis	1 -	237	( 237 aa)	50%	
Sequence 7:	A pylori	1 -	238	( 238 aa)	52%	
Sequence 8:	A heilmann	1 -	234	( 234 aa)	54%	
Alignment type:	Global Protein					
Parameters:	Mismatch 2;	Open Gap 4;	Extend Gap 1;	Conserv N		
ureXCS1	1) vkltpkeqekfllyyagevarkrkaeglklnqpeaiayisahimdearrgkktvaqilmeeecmhflkkdevmpgvqnmvpdlgveatfpdgtl1lvtvnwpiepdehfkagevkfkgcdkdi					
ureXkuka	1) .....					
ureXDS4	1) .....					
ureX2301	1) ?.....					
ureX390	1) .....ld..in..h...rl..eal..r..v..yt..v..1..grv..ek..d..n..s..d..q..grtw..en..d..as..ihev..i..n..iht..v..dnoklap..-..lkne..t					
A felis	1) m.....ld..in..h...ek..i...yv..v..1.....e...a...a..e..q..grtl..p..d..d..as..ihev..i..m.....ht..angklvp..-1..lkne..t					
A pylori	1) m.....ld..in..h...1..kg...k..i...yt..v..1.....v..e...a...s..d..q..grtl..a..d.....ah..ihev..i..g.....iht..v..agrdkl..pgevilkne..t					
A heilmann	1) m.....ld..in..h...1..kg...k..i...yt..v..1.....v..e...a...s..d..q..grtl..a..d.....ah..ihev..i..g.....iht..v..agrdkl..pgevilkne..t					
ureXCS1	121) lnadjkevteletnegpkslhvgsfffeankalkfdrekeygkrlldipsqntlrigagqtrkvqliplgskkvigmg1vnniaderhkhkaldkakshgfi-----k					
ureXkuka	121) .....					
ureXDS4	121) .....					
ureX2301	121) .....					
ureX390	121) ..V..ais..k..k..drpvq.....v..1..d...a..sfc.....a..tav..fep..eeks..e..di..n..riy..f..s..irq..adg..kig..kr..ek..gsvngceatdkd-q					
A felis	120) i...kavsvk..k..v..drpvqj.....v..rc..d.....a..tav..fep..eeks..e..di..n..riy..f..a..drq..nes..ki..hr..er..hgakssddnyvktike					
A pylori	120) i..e..havq..k..k..drpvq.....v..1..d.....a..tav..fep..eeks..e..di..n..riy..f..a..drq..hdg..kl..kr..ekh..gtlnqcdn-----					
A heilmann	121) ..havq..k..k..drpvq.....v..1..d.....a..tav..fep..eeks..e..di..n..riy..f..a..drq..hdg..kl..kr..ekh..gtlnqcdn-----					

Figure 1b

Figure 1c (1)

Figure 1c (2)

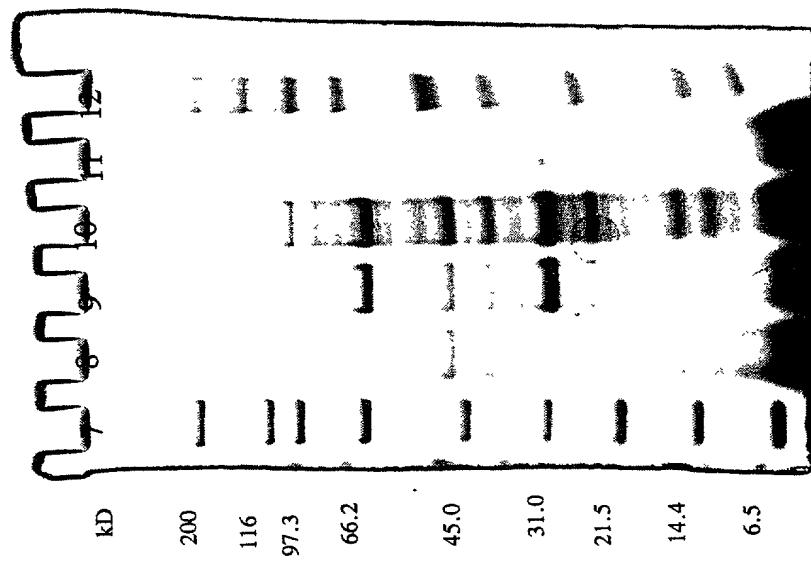


Figure 2